Campbell
Barbara
PCT

ENTERED
#5

10-12-01

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RAW SEQUENCE LISTING              DATE: 05/18/2001
PATENT APPLICATION:  US/09/830,807     TIME: 11:03:12

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 3 <110> APPLICANT: Crooke,Helen R.
 4        Clarke, Enda E.
 5        Everest, Paul H.
 6        Dougan, Gordon
 7        Holden, David W.
 8        Shea, Jacqueline E.
 9        Feldman, Robert G.
11 <120> TITLE OF INVENTION: VIRULENCE GENES AND PROTEINS, AND THEIR USE
13 <130> FILE REFERENCE: GJE-65
15 <140> CURRENT APPLICATION NUMBER: US/09/830,807
16 <141> CURRENT FILING DATE: 2001-04-30
18 <160> NUMBER OF SEQ ID NOS: 72
20 <170> SOFTWARE: PatentIn Ver. 2.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 4333
24 <212> TYPE: DNA
25 <213> ORGANISM: Escherichia coli
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (1017)..(2549)
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36 tcagaatttt ctaaattatt tctgatacgt ttgaatatcc agacgcacag cgtcgtcatg 180
38 accactaaca ccagtaaaaa ccacaggtgt gatattaatt cccaggccaa cgtattatat 240
40 ttgtcataca atgacagtcc aggccaactt tccgctttcc ctttgacgta ttgcagcata 300
42 ataaattgcg gcaatgtcag tagggggatg gctgttaaca tcgggatacc tacacgttcg 360
44 acacgtactt tccaccattt tttcaaggga tagcgtaaaa aaagcatgta ggaaaagtac 420
46 ccggatataa cgaaaaatac ctgcatgcgg aacgagtgga tgaagtcatt aaaaagggtc 480
48 agccataatg acggttcggc gctattcaca tgccatgtat ggctcgaata gattaaagaa 540
50 atatgaaaag ggatccctaa caacatcagc caggcgcgga tggagtcgag gaaatattca 600
52 cgttgcgcgg gtactgggtt catatatggt taactaatct cggattttttc gtcttatccc 660
54 tgtcgggtta tgcctttagg cttgttgcca tagcgacacc gacctgaccg cgccaggcgc 720
56 aggcttcaag gtttttatgc atagcatcat cgctaccact aaccagaatg gaagcgtctg 780
57 taagacggtt gataaataaa tttgctggca aaccctacac gaagtcgatg cttctgtctt 840
59 taggagaagc acggaaagtg aaaacggttg caatcaggtg cttaatccat gagccagtgt 900
61 gctgaacgat accgggattc tgttgtcgga atggcaggtt atccattaaa atagatcgga 960
63 tcgatataag cacacaaagg gggaagtgct tactaattat gaaacataaa ctacaa atg 1019
64                                                            Met
65                                                              1
67 atg aaa atg cgt tgg ttg agt gct gca gta atg tta acc ctg tat aca   1067
68 Met Lys Met Arg Trp Leu Ser Ala Ala Val Met Leu Thr Leu Tyr Thr
69           5               10              15
71 tct tca agc tgg gct ttc agt att gat gat gtc gca aag caa gct caa   1115
72 Ser Ser Ser Trp Ala Phe Ser Ile Asp Asp Val Ala Lys Gln Ala Gln
73        20              25              30
75 tcc tta gcc ggg aaa ggc tat gag gcg ccc aaa agc aac ttg ccc tcc   1163
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 76 Ser Leu Ala Gly Lys Gly Tyr Glu Ala Pro Lys Ser Asn Leu Pro Ser
 77      35                  40                  45
 79 gtt ttc cgc gat atg aaa tac gcg gac tat cag cag atc cag ttt aat   1211
 80 Val Phe Arg Asp Met Lys Tyr Ala Asp Tyr Gln Gln Ile Gln Phe Asn
 81 50                  55                  60                  65
 83 cat gac aaa gcg tac tgg aac aat ctg aag acc cca ttc aaa ctc gag   1259
 84 His Asp Lys Ala Tyr Trp Asn Asn Leu Lys Thr Pro Phe Lys Leu Glu
 85              70                  75                  80
 87 ttc tac cat cag ggt atg tac ttc gat acc ccg gtc aaa ata aat gaa   1307
 88 Phe Tyr His Gln Gly Met Tyr Phe Asp Thr Pro Val Lys Ile Asn Glu
 89              85                  90                  95
 91 gtg act gcc acc gca gtc aaa cga atc aaa tac agc ccg gat tat ttc   1355
 92 Val Thr Ala Thr Ala Val Lys Arg Ile Lys Tyr Ser Pro Asp Tyr Phe
 93          100                 105                 110
 95 act ttc ggc gat gtt cag cat gac aaa gac acg gta aaa gac ctt ggt   1403
 96 Thr Phe Gly Asp Val Gln His Asp Lys Asp Thr Val Lys Asp Leu Gly
 97      115                 120                 125
 99 ttt gcc ggt ttc aaa gtg ctt tac ccg atc aac agc aaa gat aaa aac   1451
100 Phe Ala Gly Phe Lys Val Leu Tyr Pro Ile Asn Ser Lys Asp Lys Asn
101 130                 135                 140                 145
103 gat gaa atc gtc agc atg ctc ggg gcc agc tat ttc cgc gtg att ggt   1499
104 Asp Glu Ile Val Ser Met Leu Gly Ala Ser Tyr Phe Arg Val Ile Gly
105                  150                 155                 160
107 gca ggt cag gtt tat ggc ctt tct gca cgc ggc ctg gca att gat acc   1547
108 Ala Gly Gln Val Tyr Gly Leu Ser Ala Arg Gly Leu Ala Ile Asp Thr
109              165                 170                 175
111 gcc ttg cca tcg ggt gaa gaa ttt cca cgc ttc aaa gag ttc tgg atc   1595
112 Ala Leu Pro Ser Gly Glu Glu Phe Pro Arg Phe Lys Glu Phe Trp Ile
113          180                 185                 190
115 gag cgt cca aaa ccg act gat aaa cgt tta acc att tat gca ttg ctt   1643
116 Glu Arg Pro Lys Pro Thr Asp Lys Arg Leu Thr Ile Tyr Ala Leu Leu
117      195                 200                 205
119 gac tcg ccg cgc gcg aca ggt gct tac aaa ttc gta gtt atg cca gga   1691
120 Asp Ser Pro Arg Ala Thr Gly Ala Tyr Lys Phe Val Val Met Pro Gly
121 210                 215                 220                 225
123 cgt gac acg gtt gtg gat gtg cag tcg aaa atc tat ctg cgc gat aaa   1739
124 Arg Asp Thr Val Val Asp Val Gln Ser Lys Ile Tyr Leu Arg Asp Lys
125              230                 235                 240
127 gtc ggc aaa ctg ggg gtt gca ccg tta acc agt atg ttc ctg ttt ggg   1787
128 Val Gly Lys Leu Gly Val Ala Pro Leu Thr Ser Met Phe Leu Phe Gly
129              245                 250                 255
131 ccg aac caa ccg tcg cct gca aat aac tat cgt ccg gag ttg cac gac   1835
132 Pro Asn Gln Pro Ser Pro Ala Asn Asn Tyr Arg Pro Glu Leu His Asp
133          260                 265                 270
135 tct aac ggt ctg tct atc cat gct ggt aat ggc gaa tgg atc tgg cgt   1883
136 Ser Asn Gly Leu Ser Ile His Ala Gly Asn Gly Glu Trp Ile Trp Arg
137      275                 280                 285
139 ccg ttg aat aac ccg aaa cat tta gcg gtc agc agc ttc tcg atg gaa   1931
140 Pro Leu Asn Asn Pro Lys His Leu Ala Val Ser Ser Phe Ser Met Glu
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141 290                 295                 300                 305
143 aac ccg caa ggc ttc ggt cta ttg cag cgt ggt cgt gat ttc tcc cgc   1979
144 Asn Pro Gln Gly Phe Gly Leu Leu Gln Arg Gly Arg Asp Phe Ser Arg
145             310                 315                 320
147 ttt gaa gat ctc gat gat cgt tac gat ctt cgt cca agc gca tgg gtg   2027
148 Phe Glu Asp Leu Asp Asp Arg Tyr Asp Leu Arg Pro Ser Ala Trp Val
149             325                 330                 335
151 act ccg aaa ggg gag tgg ggc aaa ggc agc gtt gag ctg gtg gaa att   2075
152 Thr Pro Lys Gly Glu Trp Gly Lys Gly Ser Val Glu Leu Val Glu Ile
153         340                 345                 350
155 cca acc aac gat gaa acc aac gat aac atc gtc gct tac tgg acg ccg   2123
156 Pro Thr Asn Asp Glu Thr Asn Asp Asn Ile Val Ala Tyr Trp Thr Pro
157     355                 360                 365
159 gat cag ctg ccg gag ccg ggt aaa gag atg aac ttt aaa tac acc atc   2171
160 Asp Gln Leu Pro Glu Pro Gly Lys Glu Met Asn Phe Lys Tyr Thr Ile
161 370                 375                 380                 385
163 acc ttc agc cgt gat gaa gac aaa ctg cat gcg cca gat aac gca tgg   2219
164 Thr Phe Ser Arg Asp Glu Asp Lys Leu His Ala Pro Asp Asn Ala Trp
165             390                 395                 400
167 gtg caa caa acg cgt cgt tca acg ggg gat gtg aag cag tcg aac ctg   2267
168 Val Gln Gln Thr Arg Arg Ser Thr Gly Asp Val Lys Gln Ser Asn Leu
169         405                 410                 415
171 att cgc cag cct gac ggt act atc gcc ttt gtg gtc gat ttt acc ggc   2315
172 Ile Arg Gln Pro Asp Gly Thr Ile Ala Phe Val Val Asp Phe Thr Gly
173         420                 425                 430
175 gct gag atg aaa aaa ctg cca gag gat acc ccg gtc aca gcg caa acc   2363
176 Ala Glu Met Lys Lys Leu Pro Glu Asp Thr Pro Val Thr Ala Gln Thr
177     435                 440                 445
179 agc att ggt gat aat ggt gag ata gtt gaa agc acg gtg cgt tat aac   2411
180 Ser Ile Gly Asp Asn Gly Glu Ile Val Glu Ser Thr Val Arg Tyr Asn
181 450                 455                 460                 465
183 ccg gtt acc aaa ggc tgg cgt ctg gtg atg cgt gtg aaa gtg aaa gat   2459
184 Pro Val Thr Lys Gly Trp Arg Leu Val Met Arg Val Lys Val Lys Asp
185             470                 475                 480
187 gcc aag aaa acc act gaa atg cgt gct gcg ctg gtg aat gcc gat cag   2507
188 Ala Lys Lys Thr Thr Glu Met Arg Ala Ala Leu Val Asn Ala Asp Gln
189             485                 490                 495
191 acg ttg agt gaa acc tgg agc tac cag tta cct gcc aat gaa           2549
192 Thr Leu Ser Glu Thr Trp Ser Tyr Gln Leu Pro Ala Asn Glu
193         500                 505                 510
195 taagacaact gagtacattg acgcaatgcc catcgccgca agcgagaaag cggcattgcc 2609
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249 cgttgaccga accgcaatac ttcctgcaac cacggcagtt gttcccggta tggccgcagt 4229
251 ggcgtcctga gctggcgatt gcactttttg cttcgaccat ggtgctgttg ttcctgccga 4289
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266              20                  25                  30
268 Gln Ser Leu Ala Gly Lys Gly Tyr Glu Ala Pro Lys Ser Asn Leu Pro
269          35                  40                  45
271 Ser Val Phe Arg Asp Met Lys Tyr Ala Asp Tyr Gln Gln Ile Gln Phe
272      50                  55                  60
274 Asn His Asp Lys Ala Tyr Trp Asn Asn Leu Lys Thr Pro Phe Lys Leu
275  65                  70                  75                  80
277 Glu Phe Tyr His Gln Gly Met Tyr Phe Asp Thr Pro Val Lys Ile Asn
278              85                  90                  95
280 Glu Val Thr Ala Thr Ala Val Lys Arg Ile Lys Tyr Ser Pro Asp Tyr
281          100                 105                 110
283 Phe Thr Phe Gly Asp Val Gln His Asp Lys Asp Thr Val Lys Asp Leu
284          115                 120                 125
286 Gly Phe Ala Gly Phe Lys Val Leu Tyr Pro Ile Asn Ser Lys Asp Lys
287      130                 135                 140
289 Asn Asp Glu Ile Val Ser Met Leu Gly Ala Ser Tyr Phe Arg Val Ile
290 145                 150                 155                 160
292 Gly Ala Gly Gln Val Tyr Gly Leu Ser Ala Arg Gly Leu Ala Ile Asp
293              165                 170                 175
295 Thr Ala Leu Pro Ser Gly Glu Glu Phe Pro Arg Phe Lys Glu Phe Trp
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RAW SEQUENCE LISTING   DATE: 05/18/2001
PATENT APPLICATION: US/09/830,807   TIME: 11:03:12

Input Set : A:\gje-65.txt
Output Set: N:\CRF3\05182001\I830807.raw

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305 225              230              235              240
307 Lys Val Gly Lys Leu Gly Val Ala Pro Leu Thr Ser Met Phe Leu Phe
308              245              250              255
310 Gly Pro Asn Gln Pro Ser Pro Ala Asn Asn Tyr Arg Pro Glu Leu His
311              260              265              270
313 Asp Ser Asn Gly Leu Ser Ile His Ala Gly Asn Gly Glu Trp Ile Trp
314              275              280              285
316 Arg Pro Leu Asn Asn Pro Lys His Leu Ala Val Ser Ser Phe Ser Met
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319 Glu Asn Pro Gln Gly Phe Gly Leu Leu Gln Arg Gly Arg Asp Phe Ser
320 305              310              315              320
322 Arg Phe Glu Asp Leu Asp Asp Arg Tyr Asp Leu Arg Pro Ser Ala Trp
323              325              330              335
325 Val Thr Pro Lys Gly Glu Trp Gly Lys Gly Ser Val Glu Leu Val Glu
326              340              345              350
328 Ile Pro Thr Asn Asp Glu Thr Asn Asp Asn Ile Val Ala Tyr Trp Thr
329              355              360              365
331 Pro Asp Gln Leu Pro Glu Pro Gly Lys Glu Met Asn Phe Lys Tyr Thr
332      370              375              380
334 Ile Thr Phe Ser Arg Asp Glu Asp Lys Leu His Ala Pro Asp Asn Ala
335 385              390              395              400
337 Trp Val Gln Gln Thr Arg Arg Ser Thr Gly Asp Val Lys Gln Ser Asn
338              405              410              415
340 Leu Ile Arg Gln Pro Asp Gly Thr Ile Ala Phe Val Val Asp Phe Thr
341              420              425              430
343 Gly Ala Glu Met Lys Lys Leu Pro Glu Asp Thr Pro Val Thr Ala Gln
344         435              440              445
346 Thr Ser Ile Gly Asp Asn Gly Glu Ile Val Glu Ser Thr Val Arg Tyr
347      450              455              460
349 Asn Pro Val Thr Lys Gly Trp Arg Leu Val Met Arg Val Lys Val Lys
350 465              470              475              480
352 Asp Ala Lys Lys Thr Thr Glu Met Arg Ala Ala Leu Val Asn Ala Asp
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VERIFICATION SUMMARY   DATE: 05/18/2001
PATENT APPLICATION: US/09/830,807   TIME: 11:03:13

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Output Set: N:\CRF3\05182001\I830807.raw

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L:16   M:271 C: Current Filing Date differs, Replaced Current Filing Date
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L:875  M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10
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